

SEQUENCE LISTING

<110> Seoul National University Industry Foundation
<120> ROOT-SPECIFIC EXPASIN GENE REGULATING ROOT GROWTH
AND OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
<130> OP03-0015
<150> KR 2003-19069
<151> 2003-03-27

<160> 9
<170> KopatentIn 1.71
<210> 1
<211> 1089
<212> DNA
<213> Glycine max
<220>
<221> CDS
<222> (52)..(816)
<223> Glycine max expansin (GmEXP1)

<400> 1
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atg ggc aaa atc atg ctt gtt ttg ggt agc ctc att gga tta tgc tgt 99
Met Gly Lys Ile Met Leu Val Leu Gly Ser Leu Ile Gly Leu Cys Cys
1 5 10 15
ttc aca atc act acc tat gcc ttc tca cct tct gga tgg acc aac gcc 147
Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
20 25 30
cat gcc act ttt tat ggg ggt agt gat gct tca gga act atg ggg gga 195
His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly
35 40 45
gct tgt ggg tat ggg aat ctg tat gca act ggg tat gga act aga act 243
Ala Cys Gly Tyr Gly Asn Leu Tyr Ala Thr Gly Tyr Gly Thr Arg Thr
50 55 60
gca gct tta agc act gcc tta ttt aat gat gga gct tcc tgt ggt cag 291
Ala Ala Leu Ser Thr Ala Leu Phe Asn Asp Gly Ala Ser Cys Gly Gln
65 70 75 80
tgc tac aaa att ata tgt gat tac aaa tca gac tct aga tgg tgc atc 339
Cys Tyr Lys Ile Ile Cys Asp Tyr Lys Ser Asp Ser Arg Trp Cys Ile
85 90 95

aaa gga aga tct gta acc gta act gcc aca aac ttt tgc cct ccc aat 387
 Lys Gly Arg Ser Val Thr Val Thr Ala Thr Asn Phe Cys Pro Pro Asn
 100 105 110
 ttc gcc ctt cct aac aac aat gga ggc tgg tgc aac cca cca ctc aag 435
 Phe Ala Leu Pro Asn Asn Asn Gly Gly Trp Cys Asn Pro Pro Leu Lys
 115 120 125
 cat ttt gat atg gcc caa ccc gct tgg gaa aag att ggt att tac aga 483
 His Phe Asp Met Ala Gln Pro Ala Trp Glu Lys Ile Gly Ile Tyr Arg
 130 135 140
 gga ggg atc gtc ccc gtg cta ttt caa agg gtt cca tgc aaa aag cat 531
 Gly Gly Ile Val Pro Val Leu Phe Gln Arg Val Pro Cys Lys Lys His
 145 150 155 160
 gga ggg gtt agg ttc agt gtg aat ggg agg gac tac ttt gag cta gta 579
 Gly Gly Val Arg Phe Ser Val Asn Gly Arg Asp Tyr Phe Glu Leu Val
 165 170 175
 ttg atc agc aat gtg ggg ggt gct gga tcc atc caa tca gtg ttc att 627
 Leu Ile Ser Asn Val Gly Gly Ala Gly Ser Ile Gln Ser Val Phe Ile
 180 185 190
 aaa ggc tca aaa act gga tgg atg gca atg tca aga aat tgg ggt tct 675
 Lys Gly Ser Lys Thr Gly Trp Met Ala Met Ser Arg Asn Trp Gly Ser
 195 200 205
 aat tgg caa tcc aat gcg tat ttg aat ggt caa tct ttg tcc ttc agg 723
 Asn Trp Gln Ser Asn Ala Tyr Leu Asn Gly Gln Ser Leu Ser Phe Arg
 210 215 220
 gtc acc acc act gat gga gag acc aga gtt ttc caa gat att gtt cca 771
 Val Thr Thr Thr Asp Gly Glu Thr Arg Val Phe Gln Asp Ile Val Pro
 225 230 235 240
 gta agt tgg aca ttc ggc caa act ttc tct agc cca gtt cag ttc taag 820
 Val Ser Trp Thr Phe Gly Gln Thr Phe Ser Ser Pro Val Gln Phe
 245 250 255
 ctgattacag ataaaccaac caacggctga ggcgtgcittt tttattttat tactggagct 880
 gccccccacc cttctctgg ttttgattat tcccatcaac tccaaaggct ctatcaaggc 940
 ataaattctt atcaataata caatcaatca ccatcatatc atcataagct tgtatataa 1000
 ataaacatct ttcaagttta aattaattta tactataat tgttgtataa tcattatagt 1060
 tgaagttcaa aaaaaaaaaa aaaaaaaaaa 1089

<210> 2
 <211> 255
 <212> PRT
 <213> Glycine max

<400> 2
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 1 5 10 15
 Phe Thr Ile Thr Thr Tyr Ala Phe Ser Pro Ser Gly Trp Thr Asn Ala
 20 25 30
 His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly
 35 40 45
 Ala Cys Gly Tyr Gly Asn Leu Tyr Ala Thr Gly Tyr Gly Thr Arg Thr

50	55	60													
Ala	Ala	Leu	Ser	Thr	Ala	Leu	Phe	Asn	Asp	Gly	Ala	Ser	Cys	Gly	Gln
65					70				75						80
Cys	Tyr	Lys	Ile	Ile	Cys	Asp	Tyr	Lys	Ser	Asp	Ser	Arg	Trp	Cys	Ile
					85				90						95
Lys	Gly	Arg	Ser	Val	Thr	Val	Thr	Ala	Thr	Asn	Phe	Cys	Pro	Pro	Asn
					100				105						110
Phe	Ala	Leu	Pro	Asn	Asn	Asn	Gly	Gly	Trp	Cys	Asn	Pro	Pro	Leu	Lys
	115				120							125			
His	Phe	Asp	Met	Ala	Gln	Pro	Ala	Trp	Glu	Lys	Ile	Gly	Ile	Tyr	Arg
					130				135				140		
Gly	Gly	Ile	Val	Pro	Val	Leu	Phe	Gln	Arg	Val	Pro	Cys	Lys	Lys	His
	145				150				155				160		
Gly	Gly	Val	Arg	Phe	Ser	Val	Asn	Gly	Arg	Asp	Tyr	Phe	Glu	Leu	Val
		165			170				175						
Leu	Ile	Ser	Asn	Val	Gly	Gly	Ala	Gly	Ser	Ile	Gln	Ser	Val	Phe	Ile
					180				185				190		
Lys	Gly	Ser	Lys	Thr	Gly	Trp	Met	Ala	Met	Ser	Arg	Asn	Trp	Gly	Ser
					195				200				205		
Asn	Trp	Gln	Ser	Asn	Ala	Tyr	Leu	Asn	Gly	Gln	Ser	Leu	Ser	Phe	Arg
					210				215				220		
Val	Thr	Thr	Asp	Gly	Glu	Thr	Arg	Val	Phe	Gln	Asp	Ile	Val	Pro	
	225				230				235				240		
Val	Ser	Trp	Thr	Phe	Gly	Gln	Thr	Phe	Ser	Ser	Pro	Val	Gln	Phe	
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<210> 3
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 3
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<210> 4
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 4

<210> 5
 <211> 519
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Probe

<400> 5
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 ggnacnmgna cngcngcnyt nwsnacngcn ytnttyaayg ayggngcnws ntgyggncar 120
 tgytayaara thathtgyga ytayaarwsn gaywsnmgt ggtgyathaa rggnmgnwsn 180
 gtnacngtna cngcnacnaa ytttgycn ccnaayttg cnytnccnaa yaayaayggn 240
 ggntggtya ayccnccnyt naarcaytty gayatggcnc arccngcntg ggaraarath 300
 ggnathtaym gnggnggnat hgtncngtn ytnntycarm gngtnccntg yaaraarcay 360
 gngngngtnm gnttysngt naayggnmgn gaytayttg arytngtnyt nathwsnaay 420
 gtngggngng cnggnwsnat hcarwsngtn ttyathaarg gnwsnaarac nggntggatg 480
 gcnatgwsnm gnaaytgggg nwsnaaytgg carwsnaay 519

<210> 6
 <211> 269
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> RNA probe(antisense)

<400> 6
 aauaaaaauaa aaaagcacgc cucagccuu gguugguuua ucuguaauca gcuuagaacu 60
 gaacugggcu agagaaaguu uggccgaaug uccaacuuac uggaacaaua ucuuuggaaaa 120
 cucuggucuc uccaucagug guggugaccc ugaaggacaa agauugacca uucaaauacg 180
 cauuggauug ccaauuagaa ccccaauuuc uugacauugc cauccaucca guuuuugagc 240
 cuuuuaugaa cacugauugg auggaucca 269

<210> 7
 <211> 389
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> RNA probe(sense)

<400> 7
uggauccaue caaucagugu ucauuuaagg cuaaaaacu ggauggaugg caaugucaag 60
aaauuggggu ucuauuuggc aauccaaue guauuugaaau ggucaaucuu uguccuucag 120
ggucaccacc acugauuggag agaccagagu uuuccaagau auuguuccag uaaguuggac 180
auucggccaa acuuuucucua gcccaguua guucuaagcu gauuacagau aaaccaacca 240
acggcugagg cgugcuuuuu uauuuuauua cuggagcugc ccgccacccu ucuucugguu300
uugauuauuc ccaucaacuc caagccucu aucaaggcau aaauucuuau caauaaauaca 360
aucaaucacc aucauaucu cauaagcuu 389

<210> 8
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
accaagcttc aacctctcat cattaggc 28

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
accaagcttg gagttgatgg gaataatca 29